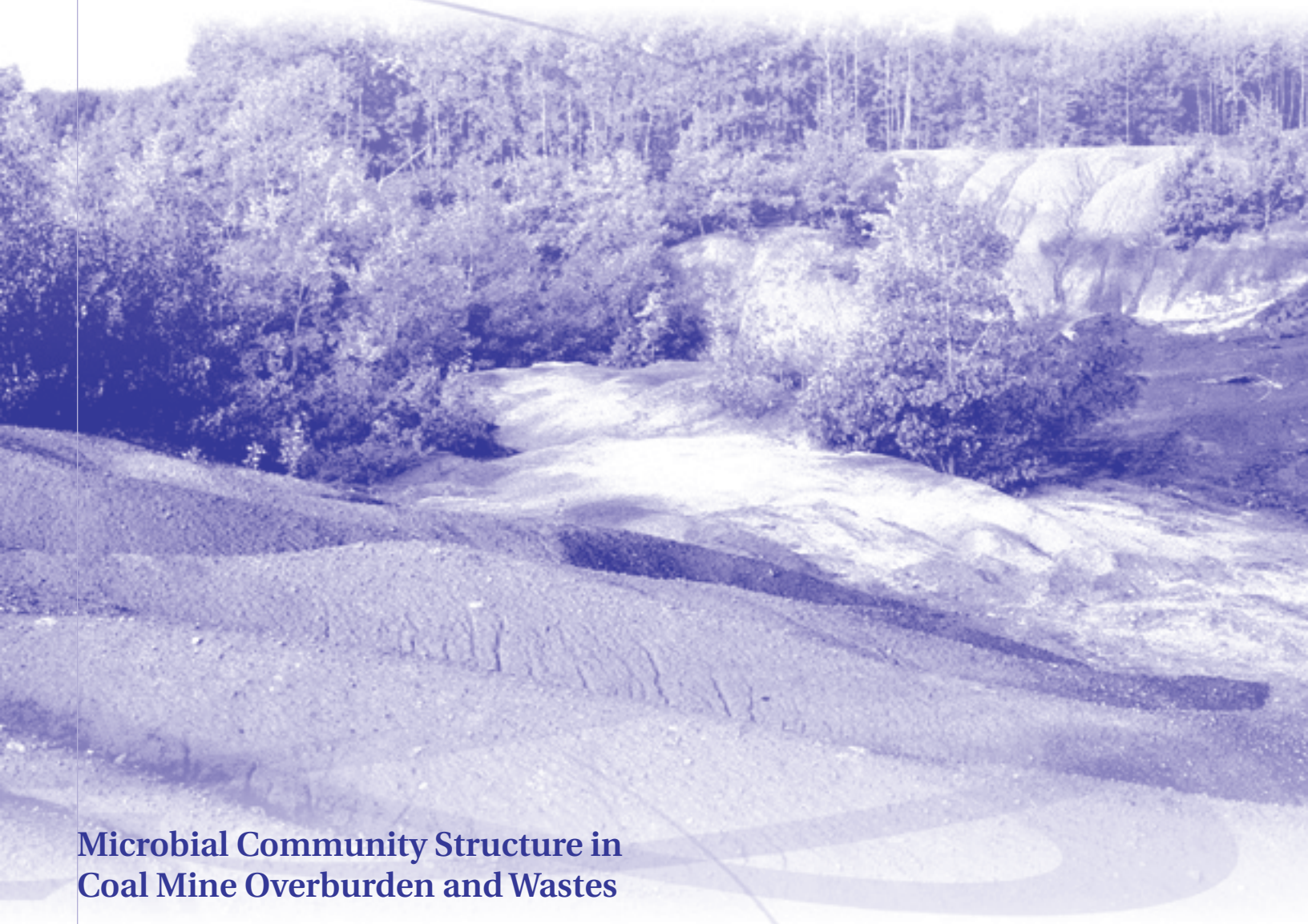
OARDC Research Enhancement
Competitive Grants Program

SEEDS
Number 4



Microbial Community Structure in Coal Mine Overburden and Wastes

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Abandoned coal mines produce and release sulfur compounds (including sulfuric acid) and other wastes that negatively impact the environment, including many streams and rivers in Ohio. Sulfuric acid production, in particular, is a result of bacterial action. Consequently, a better understanding of the bacteria involved in acid production will help improve coal mine reclamation efforts. Using new biotechnology tools, we identified twenty potentially important bacterial species found in acid-producing coal wastes. Two new bacterial species were discovered and work is being done to describe these and the other species found in the samples.

OBJECTIVES

- Extract DNA from the bacteria found in the materials above the coal seam (coal spoils) that are removed when the coal is mined during surface mining and from coal wash wastes.

- Use these data to identify the bacterial species that exist in the coal mine waste products

CHALLENGES

The biggest challenge in this work was to develop procedures that would remove soluble iron so that extraction of DNA could be successfully accomplished. Iron must be removed so that DNA extraction could proceed without interference by the iron.

ACHIEVEMENTS

We developed procedures to extract DNA from coal wastes. The DNA was then used to identify bacterial species. This work has shown us that there exists a bacterial community that was not previously known. How each bacterial species functions and interacts has yet to be discovered.

THE FUTURE

As part of a U.S. Department of Agriculture International Collaborative Grant with China, Dr. Dick visited the Huazhong Agricultural University, Wuhan, China. Professor Junchu Zhou has developed a technique to isolate single bacterial cells. Professor Zhou will come to Ohio State University for a four-month visit to collaborate with OARDC researchers on this project. Use of Professor Zhou's technique will help us identify the bacterial species found in surface coal mines. With a better understanding of the bacterial communities, our ability to improve the efficiency of reclamation is significantly increased.

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This research was funded through the OARDC Research Enhancement Competitive Grants Program, which receives funding from dollars appropriated by the state of Ohio.

design: Jesse R. Ewing photography: Warren Dick

June 2001 RECGP FS4